

From Page No. 9

Sample	abs	abs		280.1 nm	280.1 nm
11	280.0 nm	280.0 nm		280.0 nm	280.1 nm
211	0.0039	0.0030	.42	1.3013	0.5545
212	0.0471	0.0236	1.18	1.8491	0.5429
213	0.0412	0.0037	1.03	1.8151	0.5509
214	0.0331	0.0002	1.30	1.7280	0.5304
215	0.0076	0.0007	.45	1.8548	0.5457
216	0.0587	0.0075	1.47	1.5785	0.5543
217	0.0519	0.0038	1.30	1.7900	0.5577
218	0.0580	0.0216	.46	1.7857	0.5634
219	0.0533	0.0099	1.31	1.7542	0.5701
220	0.0485	0.0036	1.24	1.7194	0.5818
221	0.0438	0.0092	1.22	1.8709	0.5885
222	0.0486	0.0049	1.22	1.3529	0.7174
223	0.0271	0.0187	.63	1.4430	0.5901
224	0.0216	0.0156	.55	1.4011	0.7136
225	0.0380	0.0249	.45	1.5081	0.5543
226	0.0232	0.0150	.59	1.4827	0.5334
227	0.0357	0.0227	.49	1.5720	0.5681
228	0.0532	0.0018	1.31	1.8695	0.5936
229	0.0557	0.0064	1.39	1.5700	0.5552
230	0.0554	0.0042	1.34	1.8198	0.6174

X

DNA SEQUENCING REQUEST
Microchemistry Department

Requested by Aaron Smith Date _____
 Notebook Reference/assay: 95-1057 P. _____ Project: R
 Vector: pBc/MV Host: _____ # of Clones 20
 (Please indicate size)
 Names of Sample(s): MB 211-230 (20 samples) (OD₆₀₀ or titer)
 (Please provide OD₆₀₀ and insert size)

MB 211	MC 19209	Human sapiens cDNA 3' end	94 % (295/260)	T
212	19209	Human ABL gene, intron 1b, partial seq.	75 % (48/129)	U
213	19210	Lecithin: cholesterol acyl transferase	100 % (283/283)	T
214	19211	Human type IV collagenase mRNA	99 % (779/281)	J
215	19212	Human nephropontin mRNA	100 % (283/283)	M
216	19213	Ganglioside GM2 activator precursor (human)	96 % (236/244)	R
217	19214	Human nephropontin mRNA	99 % (281/283)	M
218	19215	Human glycoprotein mRNA	68 % (178/258)	M
219				
220	19217	Human nephropontin mRNA	98 % (275/280)	M
221				
222	19219	Human lipocortin II mRNA	59 % (96/109)	T
223	19220	Human sapiens cDNA clone 53128 3'	97 % (88/90)	R
224	19221	Human osteopontin mRNA	99 % (279/281)	J

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Witnessed & Understood by me, _____

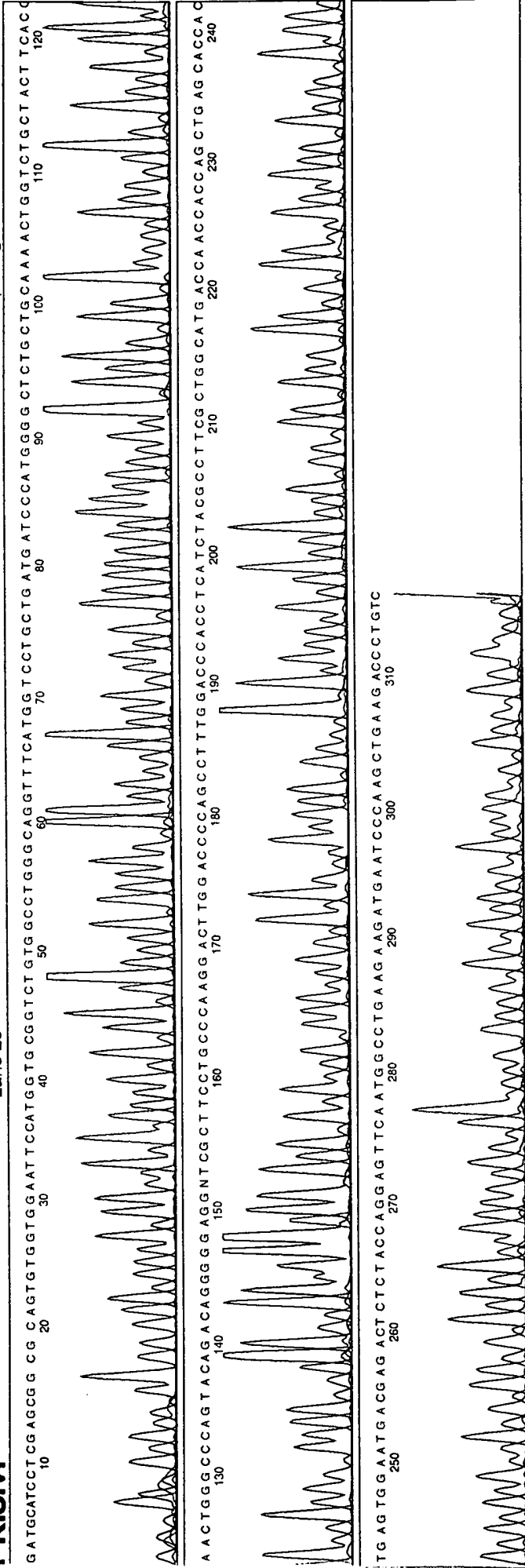
Date _____

Invented by _____

Date _____

Recorded by Aaron T. Smith

Spacing: 0.0



cc:Mail for: heather pearson

Subject: No subject given

Forwarded: JEFF GARDIN

To: Heather Pearson

To: Aaron_Smith_at_ICOS-Science@icos.com

Subject: Re: 19215

gb M80927 HUMHA3G	Human glycoprotein mRNA, complete cds.	572	4.8e-40	1
gb U19900 SSU19900	Sus scrofa 38kDa heparin-binding gly...	546	7.1e-38	1
gb R55530 R55530	yj79c12.r1 Homo sapiens cDNA clone 1...	368	2.3e-21	1
dbj D32218 HAMOSG	Hamster mRNA for oviduct-specific gl...	271	8.1e-13	1
gb U09550 HSU09550	Human oviductal glycoprotein mRNA, c...	267	1.8e-12	1
gb U17988 OAU17988	Ovis aries 92kD oestrus-associated o...	235	9.0e-10	1
dbj D16639 BOV95BOGP	Bovine mRNA for 95 kDa oviduct-speci...	217	3.1e-08	1
gb U15048 MAU15048	Mesocricetus auratus oviductin mRNA,...	211	1.0e-07	1
gb R03212 R03212	pk05a03.s1 Caenorhabditis briggsae c...	201	4.5e-07	1
gb U13646 CELZK783	Caenorhabditis elegans cosmid ZK783.	129	0.58	1
gb T92100 T92100	ye01h11.r1 Homo sapiens cDNA clone 1...	123	0.91	1

>gb|M80927|HUMHA3G Human glycoprotein mRNA, complete cds.

Length = 1741

Plus Strand HSPs:

Score = 572 (158.1 bits), Expect = 4.8e-40, P = 4.8e-40

Identities = 178/258 (68%), Positives = 178/258 (68%), Strand = Plus / Plus

Query: 24 CAGGTTTCATGGTCCTGCTGATGATCCCATGGGGCTCTGCTGCAAACTGGTCTGCTACT 83
||||| ||| ||||||| ||| ||| ||| ||||||| ||||||| ||||||| |||||||

Sbjct: 94 CAGGCTTTGTGGTCCTGGTGCTGCTCCAGTGCTGCTCTGCATACAACTGGTCTGCTACT 153

Query: 84 TCACCAACTGGGCCCAGTACAGACAGGGGGAGGNTCGCTTCCTGCCCAAGGACTTGGACC 143
||||| ||| ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 154 ACACCAGCTGGTCCCAGTACCGGGAAGGCGATGGGAGCTGCTTCCCAGATGCCCTTGACC 213

Query: 144 CCAGCCTTTGGACCCACCTCATCTACGCCTTCGCTGGCATGACCAACCACAGCTGAGCA 203
| ||| ||| ||||||| ||||||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 214 GCTTCCTCTGTACCCACATCATCTACAGCTTTGCCAATATAAGCAACGATCACATCGACA 273

Query: 204 CCACTGAGTGGAATGACGAGACTCTTACCAGGAGTTCAATGGCCTGAAGAAGATGAATC 263
|| ||| ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 274 CCTGGGAGTGGAATGATGTGACGCTCTACGGCATGCTCAACACACTCAAGAACAGGAACC 333

Query: 264 CCAAGCTGAAGACCCTGT 281
||| ||| ||| ||| |||

Sbjct: 334 CCAACCTGAAGACTCTCT 351

>gb|U19900|SSU19900 Sus scrofa 38kDa heparin-binding glycoprotein mRNA,
complete cds. >emb|Z47803|SSGP38KD S.scrofa 38kDa heparin-binding
glycoprotein.
Length = 1733

Plus Strand HSPs:

Score = 546 (150.9 bits), Expect = 7.1e-38, P = 7.1e-38

Identities = 184/278 (66%), Positives = 184/278 (66%), Strand = Plus / Plus

Query: 2 ATGGTGCGGTCTGTGGCCTGGGCAGGTTTCATGGTCTCTGCTGATGATCCCATGGGGCTCT 61
||||| ||| ||||||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 67 ATGGGTCTGAGGGTGGCTCAGACAGGTTTTGTGGCCCTGGTCTGCTCCAGAGCTGTGCT 126

Query: 62 GCTGCAAACTGGTCTGCTACTTCACCAACTGGGCCCAGTACAGACAGGGGGAGGNTCGC 121